

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	510	387.3

FIG. 1A

4D5 10 20 30 40 50
 DIVMTQSHKFMSTSVGDRVSTCKASQDVNTAVAWYQQKPGHSPKLLIYSASFRYT
 HU4D5 DIQMTQSPSSLASAVGDRVTTTCRASQDVNTAVAWYQQKPGKAPKLLIYASFLS
 HUV_LκI DIQMTQSPSSLASAVGDRVTTTCRASQDVSSYLAWYQQKPGKAPKLLIYAASSLES

 V_L-CDR1 V_L-CDR2

6639055

4D5 60 70 80 90 100
 GVPDRFTGNRSGTDTFTTSSVQAE DLAVYCCQGHYTTPTTFGGGTKLEIKRA
 HU4D5 GVPDRFTGNRSGTDTFTTSSVQAE DLAVYCCQGHYTTPTTFGGGTKLEIKRT
 HUV_LκI GVPDRFTGNRSGTDTFTTSSVQAE DLAVYCCQGHYTTPTTFGGGTKLEIKRT

 V_L-CDR3

100 90 80 70 60 50 40 30 20 10

2

2

2

VH-CDR2

2

2

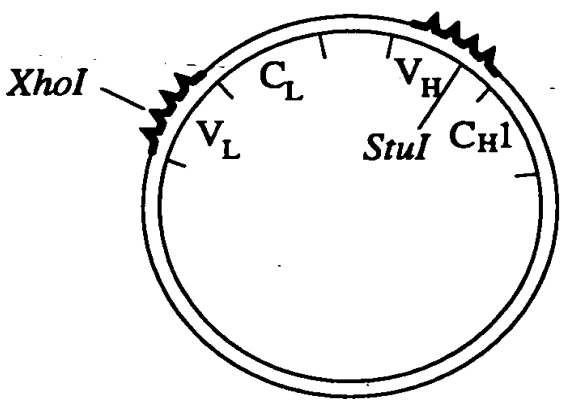
2

APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
	BY	DRAFTSMAN
	3	3

Anneal huV_L or huV_H oligomers to pAK1 template



1. Ligate
2. Isolate assembled oligomers
3. Anneal to pAK1 template (*XhoI*⁻, *StuI*⁺)
4. Extend and ligate



1. Transform *E. coli*
2. Isolate phagemid pool
3. Enrich for huV_L and huV_H (*XhoI*⁺, *StuI*⁻)
4. Sequence verify

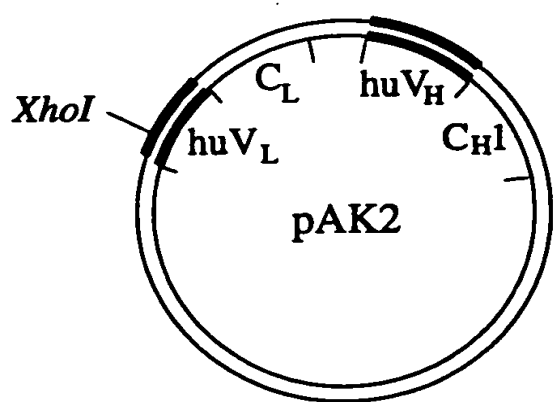


FIG. 2

APPROVED BY	O.G. FIG.	
	CLASS	SUBCLASS
DRAFTSMAN	530	387.3

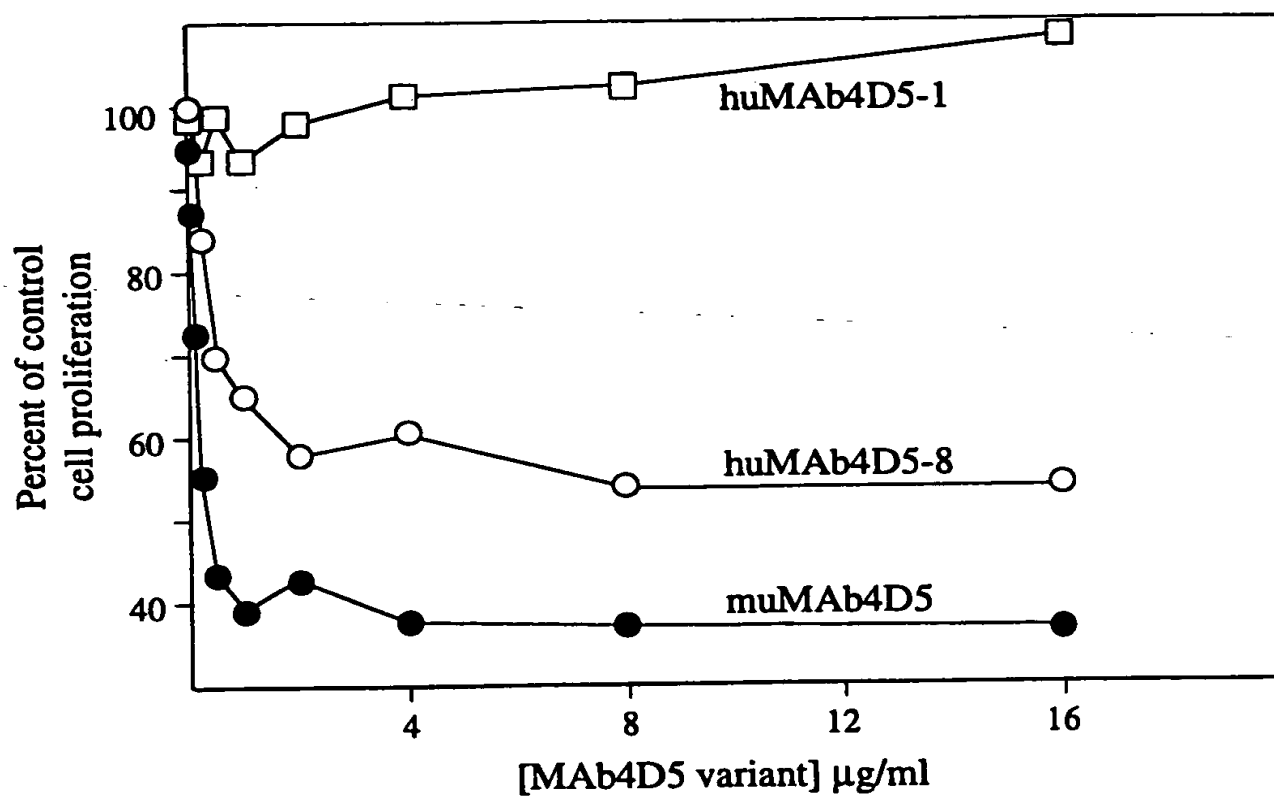


FIG. 3

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	530	387.3

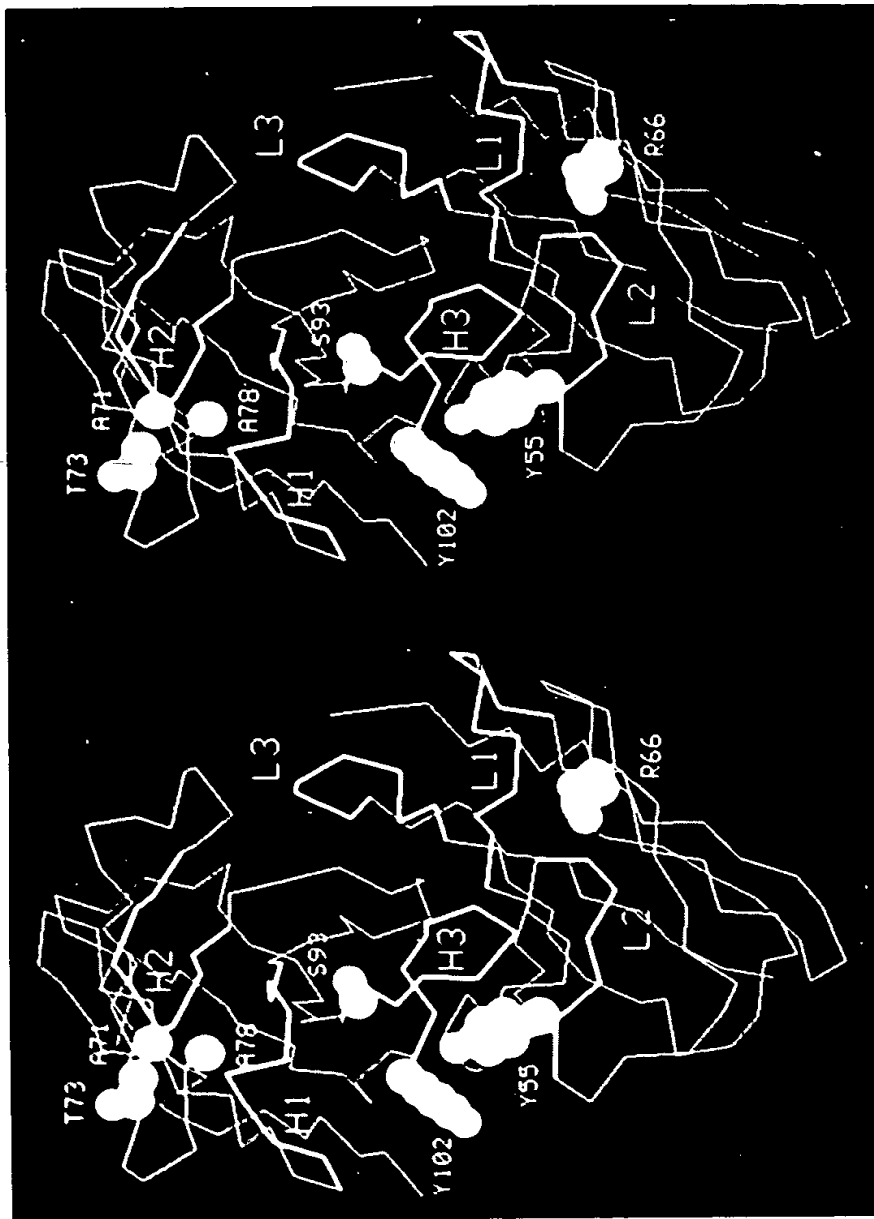


FIG. 4

APPROVED BY	O.G. FIG.	
	CLASS	SUBCLASS
DRAFTSMAN	53a	J87.3

V_L

	10	20	30	40
muxCD3	DIQMTQT	TSSLSASL	GDRVTIS	CRASQD
huxCD3v1	DIQMTQSP	SSLSASV	GDRVTIT	CRASQDIR
huκI	DIQMTQSP	SSLSASV	GDRVTIT	CRASQDIR

NYLNWYQQKP
NYLNWYQQKP
NYLNWYQQKP6
CDR-L1^^

	50	60	70	80
muxCD3	DGTVKLLI	YYTSL	HS	SGVPSK
huxCD3v1	DGTVKLLI	YYTSL	HS	SGVPSK
huκI	DGTVKLLI	YYTSL	HS	SGVPSK

FSGSGSGTDYSLTISNLEQ
FSGSGSGTDYTLTISSSLQP
FSGSGSGTDFTLTISLQP
CDR-L2

	90	100
muxCD3	EDIATYFC	QQGN
huxCD3v1	EDFATYYC	QQGN
huκI	EDFATYYC	QQGN

TLPWTFAGGTKLEIK
TLPWTFGQGTKVEIK
TLPWTFGQGTKVEIK
CDR-L3^

V_H

	10	20	30	40
muxCD3	EVQLQQSG	PELVKPG	ASMKIS	CKASGY
huxCD3v1	EVQLVESG	GGGLVQP	GGSLRL	SCAASG
huIII	EVQLVESG	GGGLVQP	GGSLRL	SCAASG

YFTGYTMNWVKQS
YFTGYTMNWVRQA
YFTGYTMNWVRQA
CDR-H1

	50	60	70
muxCD3	HGKNLEW	MGLINP	YKGVST
huxCD3v1	PGKGLEW	VALINP	YKGVST
huIII	PGKGLEW	VALINP	YKGVST

YNQKFKDKATLTVDKSSSTAY
YADSVKGRFTISVDKSKNTAY
YADSVKGRFTISRDNKNTLY
CDR-H2

	80	abc	90	100	abcde	110
muxCD3	MELLSLT	SEDS	AVYYC	ARS	GYGDS	DWYFDVWGAGTTVTVSS
huxCD3v1	LQMNSL	RAEDT	AVYYC	ARSGY	YGDSDWYFDVWGQGLTVTVSS	
huIII	LQMNSL	RAEDT	AVYYC	ARGRV	GYSLSGLYDYWGQGLTVTVSS	

DET S
CDR-H3^^

FIG. 5

APPROVED		O.G. FIG.	
BY	CLASS	SUBCLASS	
DRAFTSMAN	380	381.3	

H52H4-160

FIG. 6A-1

10 20 30
QVQLQSGPELVKPGASVKISCKTSGYTFTE

PH52-8.0

10 20 30 40 50
MGWSCILFLVATATGVHSEVQLVESGGGLVQPGGSLRLSCATSGYTFTE

H52H4-160

40 50 60 70 80
YTMHWMKQSHGKSLIEWIGGFNPKNGSSHNQRFMDKATLAVDKSTSTAYM

YTMHWMRQAPGKGLEWVAGINPKNGGTSHNQRFMDFRTISVDKSTSTAYM
60 70 80 90 100

PH52-8.0

H52H4-160

90 100 110 120 130
ELRLTSEDGIIYCARWRGLNGFDVRYFDVWGAGTTVTVSSASTKGPS

QMSLRAEDTAVYYCARWRGLNGFDVRYFDVWGAGTTVTVSSASTKGPS
110 120 130 140 150

PH52-8.0

H52H4-160

140 150 160 170 180
VFPLAPSSKSTSGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL

VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
160 170 180 190 200

PH52-8.0

H52H4-160

190 200 210 220 230
QSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTH

QSSGLYSLSSVTVTSSNFGTQTYTCNVVDHKPSNTKVDKVEPKCC---V
210 220 230 240

PH52-8.0

H52H4-160

240 250 260 270 280
TCPPCPAPPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK

ECPPCPAPP-VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQ
250 260 270 280 290

PH52-8.0

100 200 300 400 500 600 700 800 900 1000

9

9

DVQMTQTSSLSASLGDRVTINCRASQDINN
*.***.*****

10 20 30 40 50
MGMSCILFLVATATGVHSDIQMTQSPSSLASVGDVRTITCRASQDINN

```

40      50      60      70      80
YLNWYQQKPNGTVKLLIYTTSTLHSGVPSRFGSGSGTDYSLTISNLDQE
***** . ***** . . . . .
YLNWYQQKPKGAKPKLLIYTTSTLHSGVPSRFGSGSGTDYTLTISSLQPE
60      70      80      90      100

```

DIATVFCQCGNTLPPTFGGKVEIKRTVAAPSVFIFFPSDEQLKSGTAS
 *.***.*****
 DFATVYCQCGNTLPPTFGGKVEIKRTVAAPSVFIFFPSDEQLKSGTAS
 110 120 130 140 150

```

VVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLL
*****
VVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLL
160      170      180      190      200

```

SKADYEKHKVACEVTHQGLSSPVTKSFNRGEC

SKADYEKHKVACEVTHQGLSSPVTKSFNRGEC
210 220 230

210 220 230